

1600

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/654,449

DATE: 11/14/2001

TIME: 15:14:55

RECEIVED

AUG 04 2003

TECH CENTER 1600/2900

Input Set : A:\4085-226-27.ST25.txt

Output Set: N:\CRF3\11142001\I654449.raw

3 <110> APPLICANT: Palmer, Michelle A.J.  
 4 Gee, Melissa  
 5 Tillotson, Bonnie  
 6 Chang, Xiao-Jia  
 8 <120> TITLE OF INVENTION: Receptor Function Assay for G-Protein Coupled Receptors and Orphan

Receptors by Reporter Enzyme Mutant Complementation

9  
 11 <130> FILE REFERENCE: 4085-226-27  
 C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/654,449

14 &lt;141&gt; CURRENT FILING DATE: 2000-09-01

16 &lt;150&gt; PRIOR APPLICATION NUMBER: US 60/180,669

17 &lt;151&gt; PRIOR FILING DATE: 2000-02-07

19 &lt;160&gt; NUMBER OF SEQ ID NOS: 5

21 &lt;170&gt; SOFTWARE: FastSEQ for Windows Version 4.0

23 &lt;210&gt; SEQ ID NO: 1

24 &lt;211&gt; LENGTH: 6700

25 &lt;212&gt; TYPE: DNA

26 &lt;213&gt; ORGANISM: Artificial Sequence

28 &lt;220&gt; FEATURE:

29 &lt;223&gt; OTHER INFORMATION: Nucleotide sequence for pICAST ALC ✓

31 &lt;221&gt; NAME/KEY: CDS

32 &lt;222&gt; LOCATION: (1457)...(4486)

34 &lt;400&gt; SEQUENCE: 1

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35 ctgcagcctg aatatgggcc aaacaggata tctgtggtta gcagttcctg ccccggtctca 60
36 gggccaagaa cagatggaac agctgaatat gggccaaaca ggatatctgt ggtaagcagt 120
37 tcctgccccg gctcagggcc aagaacagat ggtccccaga tgcggtccag cccctcagcag 180
38 ttcttagaga accatcagat gtttccagggt tgccccagg acctgaaatg accctgtgcc 240
39 ttatttgaac taaccaatca gtctcgttct cgtttctgtt cgcgcgcttc tgcctcccca 300
40 gctcaataaa agagcccaca acccctcact cggggcgcca gtctcctgat tgactgagtc 360
41 gcccggttac ccgtgtatcc aataaaccct ctgtcagttg catccgactt gtggtctcgc 420
42 tgttccttgg gaggggtctcc tctgagtgat tgactaccgc tcagcggggg tctttcattt 480
43 gggggctcgt ccgggatcgg gagaccctcg cccaggggacc accgaccac caccgggagg 540
44 caagctggcc agcaacttat ctgtgtctgt ccgattgtct agtgtctatg actgatttta 600
45 tgcgcctgcg tcggtactag ttagctaact agctctgtat ctggcggacc cgtggtggaa 660
46 ctgacgagtt ctgaacaccc ggccgcaacc ctgggagacg tcccagggaac tttggggggc 720
47 gtttttgtgg ccgacctga ggaaggaggt cgatgtggaa tccgaccccg tcaggatatg 780
48 tggttctggt aggagacgag aacctaaaac agttcccgcc tccgtctgaa tttttgcttt 840
49 cggtttggaa ccgaagccgc gcgtcttgtc tgcgtcagca tcgttctgtg ttgtctctgt 900
50 ctgactgtgt ttctgtattt gtctgaaaat tagggccaga ctgttaccac tcccttaagt 960
51 ttgaccttag gtaactggaa agatgtcgag cggctcgtc acaaccagtc ggtagatgtc 1020
52 aagaagagac gttgggttae etttctgtct gcagaatggc caacctttta cgtcggatgg 1080
53 ccgcgagacg gcacctttta ccgagacctc atcaccagg ttaagatcaa ggtcttttca 1140
54 cctggccgcg atggacccc agacaggtc cctacatcg tgacctggga agccttggct 1200
55 tttgaccccc ctccctgggt caagcccttt gtacacccta agcctccgcc tctcttctct 1260
56 ccatccgccc cgtctctccc ccttgaacct cctcgttcga cccgcctcg atcctccctt 1320
57 tatccagccc tcaactcctt tctagcgcc ggcgcgtcta gccattaat acgactcaat 1380
58 atagggcgat tcgaatcagg ccttggcgcg ccggatcctt aattaagcgc aattgggagg 1440
59 tggcggttag ctcgag atg ggc gtg att acg gat tca ctg gcc gtc gtg gcc 1492

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TECH CENTER 1600/2900

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60           Met Gly Val Ile Thr Asp Ser Leu Ala Val Val Ala
61           1           5           10
63 cgc acc gat cgc cct tcc caa cag tta cgc agc ctg aat ggc gaa tgg 1540
64 Arg Thr Asp Arg Pro Ser Gln Gln Leu Arg Ser Leu Asn Gly Glu Trp
65           15           20           25
67 cgc ttt gcc tgg ttt ccg gca cca gaa gcg gtg ccg gaa agc tgg ctg 1588
68 Arg Phe Ala Trp Phe Pro Ala Pro Glu Ala Val Pro Glu Ser Trp Leu
69           30           35           40
71 gag tgc gat ctt cct gag gcc gat act gtc gtc gtc ccc tca aac tgg 1636
72 Glu Cys Asp Leu Pro Glu Ala Asp Thr Val Val Val Pro Ser Asn Trp
73 45           50           55           60
75 cag atg cac ggt tac gat gcg ccc atc tac acc aac gtg acc tat ccc 1684
76 Gln Met His Gly Tyr Asp Ala Pro Ile Tyr Thr Asn Val Thr Tyr Pro
77           65           70           75
79 att acg gtc aat ccg ccg ttt gtt ccc acg gag aat ccg acg ggt tgt 1732
80 Ile Thr Val Asn Pro Pro Phe Val Pro Thr Glu Asn Pro Thr Gly Cys
81           80           85           90
83 tac tcg ctc aca ttt aat gtt gat gaa agc tgg cta cag gaa ggc cag 1780
84 Tyr Ser Leu Thr Phe Asn Val Asp Glu Ser Trp Leu Gln Glu Gly Gln
85           95           100           105
87 acg cga att att ttt gat ggc gtt aac tcg gcg ttt cat ctg tgg tgc 1828
88 Thr Arg Ile Ile Phe Asp Gly Val Asn Ser Ala Phe His Leu Trp Cys
89           110           115           120
91 aac ggg cgc tgg gtc ggt tac ggc cag gac agt cgt ttg ccg tct gaa 1876
92 Asn Gly Arg Trp Val Gly Tyr Gly Gln Asp Ser Arg Leu Pro Ser Glu
93 125           130           135           140
95 ttt gac ctg agc gca ttt tta cgc gcc gga gaa aac cgc ctc gcg gtg 1924
96 Phe Asp Leu Ser Ala Phe Leu Arg Ala Gly Glu Asn Arg Leu Ala Val
97           145           150           155
99 atg gtg ctg cgc tgg agt gac ggc agt tat ctg gaa gat cag gat atg 1972
100 Met Val Leu Arg Trp Ser Asp Gly Ser Tyr Leu Glu Asp Gln Asp Met
101           160           165           170
103 tgg cgg atg agc ggc att ttc cgt gac gtc tcg ttg ctg cat aaa ccg 2020
104 Trp Arg Met Ser Gly Ile Phe Arg Asp Val Ser Leu Leu His Lys Pro
105           175           180           185
107 act aca caa atc agc gat ttc cat gtt gcc act cgc ttt aat gat gat 2068
108 Thr Thr Gln Ile Ser Asp Phe His Val Ala Thr Arg Phe Asn Asp Asp
109           190           195           200
111 ttc agc cgc gct gta ctg gag gct gaa gtt cag atg tgc ggc gag ttg 2116
112 Phe Ser Arg Ala Val Leu Glu Ala Glu Val Gln Met Cys Gly Glu Leu
113 205           210           215           220
115 cgt gac tac cta ccg gta aca gtt tct tta tgg cag ggt gaa acg cag 2164
116 Arg Asp Tyr Leu Arg Val Thr Val Ser Leu Trp Gln Gly Glu Thr Gln
117           225           230           235
119 gtc gcc agc ggc acc gcg cct ttc ggc ggt gaa att atc gat gag cgt 2212
120 Val Ala Ser Gly Thr Ala Pro Phe Gly Gly Glu Ile Ile Asp Glu Arg
121           240           245           250
123 ggt ggt tat gcc gat cgc gtc aca cta cgt ctg aac gtc gaa aac ccg 2260
124 Gly Gly Tyr Ala Asp Arg Val Thr Leu Arg Leu Asn Val Glu Asn Pro

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125	255	260	265	
127	aaa ctg tgg agc gcc gaa atc ccg aat ctc tat cgt gcg gtg gtt gaa	2308		
128	Lys Leu Trp Ser Ala Glu Ile Pro Asn Leu Tyr Arg Ala Val Val Glu			
129	270 275 280			
131	ctg cac acc gcc gac gcc acg ctg att gaa gca gaa gcc tgc gat gtc	2356		
132	Leu His Thr Ala Asp Gly Thr Leu Ile Glu Ala Glu Ala Cys Asp Val			
133	285 290 295 300			
135	ggt ttc cgc gag gtg cgg att gaa aat ggt ctg ctg ctg ctg aac gcc	2404		
136	Gly Phe Arg Glu Val Arg Ile Glu Asn Gly Leu Leu Leu Leu Asn Gly			
137	305 310 315			
139	aag ccg ttg ctg att cga gcc gtt aac cgt cac gag cat cat cct ctg	2452		
140	Lys Pro Leu Leu Ile Arg Gly Val Asn Arg His Glu His His Pro Leu			
141	320 325 330			
143	cat ggt cag gtc atg gat gag cag acg atg gtg cag gat atc ctg ctg	2500		
144	His Gly Gln Val Met Asp Glu Gln Thr Met Val Gln Asp Ile Leu Leu			
145	335 340 345			
147	atg aag cag aac aac ttt aac gcc gtg cgc tgt tcg cat tat ccg aac	2548		
148	Met Lys Gln Asn Asn Phe Asn Ala Val Arg Cys Ser His Tyr Pro Asn			
149	350 355 360			
151	cat ccg ctg tgg tac acg ctg tgc gac cgc tac gcc ctg tat gtg gtg	2596		
152	His Pro Leu Trp Tyr Thr Leu Cys Asp Arg Tyr Gly Leu Tyr Val Val			
153	365 370 375 380			
155	gat gaa gcc aat att gaa acc cac gcc atg gtg cca atg aat cgt ctg	2644		
156	Asp Glu Ala Asn Ile Glu Thr His Gly Met Val Pro Met Asn Arg Leu			
157	385 390 395			
159	acc gat gat ccg cgc tgg cta ccg gcg atg agc gaa cgc gta acg cga	2692		
160	Thr Asp Asp Pro Arg Trp Leu Pro Ala Met Ser Glu Arg Val Thr Arg			
161	400 405 410			
163	atg gtg cag cgc gat cgt aat cac ccg agt gtg atc atc tgg tcg ctg	2740		
164	Met Val Gln Arg Asp Arg Asn His Pro Ser Val Ile Ile Trp Ser Leu			
165	415 420 425			
167	ggg aat gaa tca gcc cac gcc gct aat cac gac gcg ctg tat cgc tgg	2788		
168	Gly Asn Glu Ser Gly His Gly Ala Asn His Asp Ala Leu Tyr Arg Trp			
169	430 435 440			
171	atc aaa tct gtc gat cct tcc cgc ccg gtg cag tat gaa gcc gcc gga	2836		
172	Ile Lys Ser Val Asp Pro Ser Arg Pro Val Gln Tyr Glu Gly Gly Gly			
173	445 450 455 460			
175	gcc gac acc acg gcc acc gat att att tgc ccg atg tac gcg cgc gtg	2884		
176	Ala Asp Thr Thr Ala Thr Asp Ile Ile Cys Pro Met Tyr Ala Arg Val			
177	465 470 475			
179	gat gaa gac cag ccc ttc ccg gct gtg ccg aaa tgg tcc atc aaa aaa	2932		
180	Asp Glu Asp Gln Pro Phe Pro Ala Val Pro Lys Trp Ser Ile Lys Lys			
181	480 485 490			
183	tgg ctt tcg cta cct gga gag acg cgc ccg ctg atc ctt tgc gaa tac	2980		
184	Trp Leu Ser Leu Pro Gly Glu Thr Arg Pro Leu Ile Leu Cys Glu Tyr			
185	495 500 505			
187	gcc cac gcg atg ggt aac agt ctt gcc ggt ttc gct aaa tac tgg cag	3028		
188	Ala His Ala Met Gly Asn Ser Leu Gly Gly Phe Ala Lys Tyr Trp Gln			
189	510 515 520			

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191	gcg	ttt	cgt	cag	tat	ccc	cgt	tta	cag	ggc	ggc	ttc	gtc	tgg	gac	tgg	3076
192	Ala	Phe	Arg	Gln	Tyr	Pro	Arg	Leu	Gln	Gly	Gly	Phe	Val	Trp	Asp	Trp	
193	525					530						535				540	
195	gtg	gat	cag	tcg	ctg	att	aaa	tat	gat	gaa	aac	ggc	aac	ccg	tgg	tcg	3124
196	Val	Asp	Gln	Ser	Leu	Ile	Lys	Tyr	Asp	Glu	Asn	Gly	Asn	Pro	Trp	Ser	
197						545						550				555	
199	gct	tac	ggc	ggt	gat	ttt	ggc	gat	acg	ccg	aac	gat	cgc	cag	ttc	tgt	3172
200	Ala	Tyr	Gly	Gly	Asp	Phe	Gly	Asp	Thr	Pro	Asn	Asp	Arg	Gln	Phe	Cys	
201						560						565				570	
203	atg	aac	ggt	ctg	gtc	ttt	gcc	gac	cgc	acg	ccg	cat	cca	gcg	ctg	acg	3220
204	Met	Asn	Gly	Leu	Val	Phe	Ala	Asp	Arg	Thr	Pro	His	Pro	Ala	Leu	Thr	
205						575						580				585	
207	gaa	gca	aaa	cac	cag	cag	cag	ttt	ttc	cag	ttc	cgt	tta	tcc	ggg	caa	3268
208	Glu	Ala	Lys	His	Gln	Gln	Gln	Phe	Phe	Gln	Phe	Arg	Leu	Ser	Gly	Gln	
209						590						600					
211	acc	atc	gaa	gtg	acc	agc	gaa	tac	ctg	ttc	cgt	cat	agc	gat	aac	gag	3316
212	Thr	Ile	Glu	Val	Thr	Ser	Glu	Tyr	Leu	Phe	Arg	His	Ser	Asp	Asn	Glu	
213	605					610						615				620	
215	ctc	ctg	cac	tgg	atg	gtg	gcg	ctg	gat	ggt	aag	ccg	ctg	gca	agc	ggt	3364
216	Leu	Leu	His	Trp	Met	Val	Ala	Leu	Asp	Gly	Lys	Pro	Leu	Ala	Ser	Gly	
217						625						630				635	
219	gaa	gtg	cct	ctg	gat	gtc	gct	cca	caa	ggt	aaa	cag	ttg	att	gaa	ctg	3412
220	Glu	Val	Pro	Leu	Asp	Val	Ala	Pro	Gln	Gly	Lys	Gln	Leu	Ile	Glu	Leu	
221						640						645				650	
223	cct	gaa	cta	ccg	cag	ccg	gag	agc	gcc	ggg	caa	ctc	tgg	ctc	aca	gta	3460
224	Pro	Glu	Leu	Pro	Gln	Pro	Glu	Ser	Ala	Gly	Gln	Leu	Trp	Leu	Thr	Val	
225						655						660				665	
227	cgc	gta	gtg	caa	ccg	aac	gcg	acc	gca	tgg	tca	gaa	gcc	ggg	cac	atc	3508
228	Arg	Val	Val	Gln	Pro	Asn	Ala	Thr	Ala	Trp	Ser	Glu	Ala	Gly	His	Ile	
229						670						675				680	
231	agc	gcc	tgg	cag	cag	tgg	cgt	ctg	gcg	gaa	aac	ctc	agt	gtg	acg	ctc	3556
232	Ser	Ala	Trp	Gln	Gln	Trp	Arg	Leu	Ala	Glu	Asn	Leu	Ser	Val	Thr	Leu	
233	685					690						695				700	
235	ccc	gcc	gcg	tcc	cac	gcc	atc	ccg	cat	ctg	acc	acc	agc	gaa	atg	gat	3604
236	Pro	Ala	Ala	Ser	His	Ala	Ile	Pro	His	Leu	Thr	Thr	Ser	Glu	Met	Asp	
237						705						710				715	
239	ttt	tgc	atc	gag	ctg	ggt	aat	aag	cgt	tgg	caa	ttt	aac	cgc	cag	tca	3652
240	Phe	Cys	Ile	Glu	Leu	Gly	Asn	Lys	Arg	Trp	Gln	Phe	Asn	Arg	Gln	Ser	
241						720						725				730	
243	ggc	ttt	ctt	tca	cag	atg	tgg	att	ggc	gat	aaa	aaa	caa	ctg	ctg	acg	3700
244	Gly	Phe	Leu	Ser	Gln	Met	Trp	Ile	Gly	Asp	Lys	Lys	Gln	Leu	Leu	Thr	
245						735						740				745	
247	ccg	ctg	cgc	gat	cag	ttc	acc	cgt	gca	ccg	ctg	gat	aac	gac	att	ggc	3748
248	Pro	Leu	Arg	Asp	Gln	Phe	Thr	Arg	Ala	Pro	Leu	Asp	Asn	Asp	Ile	Gly	
249						750						755				760	
251	<del>gta</del>	<del>agt</del>	<del>gaa</del>	<del>gcg</del>	<del>acc</del>	<del>cgc</del>	<del>att</del>	<del>gac</del>	<del>eet</del>	<del>aac</del>	<del>gcc</del>	<del>tgg</del>	<del>gtc</del>	<del>gaa</del>	<del>cgc</del>	<del>tgg</del>	3796
252	Val	Ser	Glu	Ala	Thr	Arg	Ile	Asp	Pro	Asn	Ala	Trp	Val	Glu	Arg	Trp	
253	765					770						775				780	
255	aag	gcg	gcg	ggc	cat	tac	cag	gcc	gaa	gca	gcg	ttg	ttg	cag	tgc	acg	3844

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256 Lys Ala Ala Gly His Tyr Gln Ala Glu Ala Ala Leu Leu Gln Cys Thr
257      785      790      795
259 gca gat aca ctt gct gat gcg gtg ctg att acg acc gct cac gcg tgg 3892
260 Ala Asp Thr Leu Ala Asp Ala Val Leu Ile Thr Thr Ala His Ala Trp
261      800      805      810
263 cag cat cag ggg aaa acc tta ttt atc agc cgg aaa acc tac cgg att 3940
264 Gln His Gln Gly Lys Thr Leu Phe Ile Ser Arg Lys Thr Tyr Arg Ile
265      815      820      825
267 gat ggt agt ggt caa atg gcg att acc gtt gat gtt gaa gtg gcg agc 3988
268 Asp Gly Ser Gly Gln Met Ala Ile Thr Val Asp Val Glu Val Ala Ser
269      830      835      840
271 gat aca ccg cat ccg gcg cgg att ggc ctg aac tgc cag ctg gcg cag 4036
272 Asp Thr Pro His Pro Ala Arg Ile Gly Leu Asn Cys Gln Leu Ala Gln
273 845      850      855      860
275 gta gca gag cgg gta aac tgg ctc gga tta ggg ccg caa gaa aac tat 4084
276 Val Ala Glu Arg Val Asn Trp Leu Gly Leu Gly Pro Gln Glu Asn Tyr
277      865      870      875
279 ccc gac cgc ctt act gcc gcc tgt ttt gac cgc tgg gat ctg cca ttg 4132
280 Pro Asp Arg Leu Thr Ala Ala Cys Phe Asp Arg Trp Asp Leu Pro Leu
281      880      885      890
283 tca gac atg tat acc ccg tac gtc ttc ccg agc gaa aac ggt ctg cgc 4180
284 Ser Asp Met Tyr Thr Pro Tyr Val Phe Pro Ser Glu Asn Gly Leu Arg
285      895      900      905
287 tgc ggg acg cgc gaa ttg aat tat ggc cca cac cag tgg cgc ggc gac 4228
288 Cys Gly Thr Arg Glu Leu Asn Tyr Gly Pro His Gln Trp Arg Gly Asp
289      910      915      920
291 ttc cag ttc aac atc agc cgc tac agt caa cag caa ctg atg gaa acc 4276
292 Phe Gln Phe Asn Ile Ser Arg Tyr Ser Gln Gln Gln Leu Met Glu Thr
293 925      930      935      940
295 agc cat cgc cat ctg ctg cac gcg gaa gaa ggc aca tgg ctg aat atc 4324
296 Ser His Arg His Leu Leu His Ala Glu Glu Gly Thr Trp Leu Asn Ile
297      945      950      955
299 gac ggt ttc cat atg ggg att ggt ggc gac gac tcc tgg agc ccg tca 4372
300 Asp Gly Phe His Met Gly Ile Gly Gly Asp Asp Ser Trp Ser Pro Ser
301      960      965      970
303 gta tcg gcg gaa ttc cag ctg agc gcc ggt cgc tac cat tac cag ttg 4420
304 Val Ser Ala Glu Phe Gln Leu Ser Ala Gly Arg Tyr His Tyr Gln Leu
305      975      980      985
307 gtc tgg tgt caa aaa aga tct gac tat aaa gat gag gac ctc gac cat 4468
308 Val Trp Cys Gln Lys Arg Ser Asp Tyr Lys Asp Glu Asp Leu Asp His
309      990      995      1000
311 cat cat cat cat cac cgg taataatagg tagataagtg actgattaga 4516
312 His His His His His Arg
313 1005      1010
315 tgcattgac cctcgaccaa ttccggttat ttccaccat attgccgtct tttggcaatg 4576
316 tgaggggeeg gaaacctggc cctgtcttct tgacgagcat tctaggggt ctttcccctc 4636
317 tcgccaaagg aatgcaagg ctgttgaatg tcgtgaagga agcagttcct ctggaagctt 4696
318 cttgaagaca aacaacgtct gtagegaccc tttgcaggca gcggaacccc ccacctggcg 4756
319 acaggtgcct ctgcggccaa aagccacgtg tataagatac acctgcaaag gcggcacaac 4816

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VERIFICATION SUMMARY

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L:13 M:270 C: Current Application Number differs, Replaced Current Application Number